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RAW SEQUENCE LISTING      DATE: 01/12/2001  
PATENT APPLICATION: US/09/218,913A      TIME: 10:23:22

Input Set : A:\Pto.amc  
Output Set : N:\CRF3\01112001\I218913A.raw

```

212 Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met
213           35                      40                      45
215 Leu Arg Cys
216           50
218 <210> SEQ ID NO: 8
219 <211> LENGTH: 92
220 <212> TYPE: PRT
221 <213> ORGANISM: Homo sapien
223 <400> SEQUENCE: 8
224 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
225 1           5                      10                      15
227 Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
228           20                      25                      30
230 Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser
231           35                      40                      45
233 Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
234           50                      55                      60
236 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
237 65           70                      75                      80
239 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser
240           85                      90
242 <210> SEQ ID NO: 9
243 <211> LENGTH: 708
244 <212> TYPE: DNA
245 <213> ORGANISM: Homo sapien
247 <220> FEATURE:
248 <221> NAME/KEY: misc_feature
249 <222> LOCATION: 679..708
250 <223> OTHER INFORMATION: /note= "n at positions 622, 679, 707 is any nucleic acid"
252 <400> SEQUENCE: 9
253 ggccgggtcg ttctctgcct ggcggggatc gctgctcttc lctgggggtcc tggcggccga 60
255 ccgagaacgc agcatccacq acttctgcct qgtgtcgaaq qtggtgggca gatgccgggc 120
257 ctccatgcct aggtggtggt acaatgtcac tgacggatcc tgccagctgt ttgtgtatyg 180
259 gggctgtgac ggaaacagca ataattacct gaccaaggag gagtgcctca agaaatgtgc 240
261 cactgtlcaca gagaatgccg cgggtgacct ggccaccagc aggaatgcag cggattcctc 300
263 tgtcccaagt gctccacagaa ggcaggatcc tgaagaccac tccagcgata tgttcaacta 360
265 tgaagaatac tgcaccgccg acgcagtcac tgggccttgc cgtgcatect tcccacgctg 420
267 gtactttgac gtggagagga actcctgcaa taacttcac tatggaggct gccggggcaa 480
269 taagaacagc kacgcctctg aggaggcctg catgctccgc tgcctccgcc agcaggagaa 540
271 tcctccctcg ccctctggct caaagggtgt ggttctggcc ggggctgttt cgtgatggtg 600
273 ttgatecttt tctgggggag cntccatggt cttactgatt ccgggtggca aggaggaacc 660
275 aggagcgtgc cctgcggganc gtctggagct tcggagatga caagggnt 708
277 <210> SEQ ID NO: 10
278 <211> LENGTH: 235
279 <212> TYPE: PRT
280 <213> ORGANISM: Homo sapien
282 <220> FEATURE:
283 <221> NAME/KEY: peptide
284 <222> LOCATION: 1..235

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*see next page*

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285 <223> OTHER INFORMATION: /note= "Xaa at positions 201, 226, and 233 are nonsense or stop codons"  
287 <400> SEQUENCE: 10  
288 Ala Gly Ser Phe Leu Ala Trp Leu Gly Ser Leu Leu Leu Ser Gly Val  
289 1 5 10 15  
291 Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser  
292 20 25 30  
294 Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn  
295 35 40 45  
297 Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly  
298 50 55 60  
300 Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala  
301 65 70 75 80  
303 Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala  
304 85 90 95  
306 Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp  
307 100 105 110  
309 His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala  
310 115 120 125  
312 Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val  
313 130 135 140  
315 Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn  
316 145 150 155 160  
318 Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg  
319 165 170 175  
321 Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu  
322 180 185 190  
W--> 324 Ala Gly Ala Val Ser Xaa Trp Cys Xaa Ser Phe Ser Trp Gly Ala Ser  
325 195 200 205  
327 Met Val Leu Leu Ile Pro Gly Gly Lys Glu Glu Pro Gly Ala Cys Pro  
328 210 215 220  
W--> 330 Ala Xaa Arg Leu Glu Leu Arg Arg Xaa Gln Gly  
331 225 230 235  
333 <210> SEQ ID NO: 11  
334 <211> LENGTH: 179  
335 <212> TYPE: PRT  
336 <213> ORGANISM: Homo sapien  
338 <220> FEATURE:  
339 <221> NAME/KEY: peptide  
340 <222> LOCATION: 1..170  
341 <223> OTHER INFORMATION: /note= "Xaa at positions 8, 17, 19, 21-26, 40, 42, 45-47, 52, 64,  
342 103, 112, 114, 116-121, 135, 137, 140-142, 147, and 159 is any  
343 amino acid residue"  
345 <400> SEQUENCE: 11  
W--> 346 Ala Asp Arg Glu Arg Ser Ile Xaa Asp Phe Cys Leu Val Ser Lys Val  
347 1 5 10 15  
349 Xaa Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Trp Trp Tyr Asn Val Thr  
350 20 25 30  
352 Asp Gly Ser Cys Gln Leu Phe Xaa Tyr Xaa Gly Cys Xaa Xaa Xaa Ser  
353 35 40 45

4  
invalid use of Xaa

Xaa can only represent  
a single amino acid,  
nothing else. \*

what about Xaa  
at position 198?

\*FYI, per 1.822(5)(e)  
of new Sequence Rules, "a  
sequence with a gap or gaps  
shall be presented as a plurality  
of separate  
sequences..."

FYI:

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.